

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2001, 15:34:35 ; Search time 23.63 Seconds

(Without alignments)  
669.743 Million cell updates/sec

Title: US-09-653-755a-6

Perfect score: 2487

Sequence: 1 EVQLQSGPELVKPGASVWL.....YIAKTTISRSKPGKHHHHH 462

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1802	72.5	336	1 GCB_MOUSE	P01866 mus musculu
2	1797	72.3	405	1 GCB_MOUSE	P01867 mus musculu
3	1419	57.1	330	1 GCAA_MOUSE	P01863 mus musculu
4	1414	56.9	399	1 GCAA_MOUSE	P01865 mus musculu
5	1385.5	55.7	335	1 GCB_MOUSE	P01864 mus musculu
6	1326.5	53.3	333	1 GCB_MOUSE	P01864 mus musculu
7	1202.5	48.4	329	1 GCB_MOUSE	P01864 mus musculu
8	1170	47.0	329	1 GCB_MOUSE	P01864 mus musculu
9	1159	46.6	398	1 GCB_MOUSE	P01864 mus musculu
10	1150	46.2	324	1 GCB_MOUSE	P01864 mus musculu
11	1145	46.0	393	1 GCB_MOUSE	P01864 mus musculu
12	1112	44.7	326	1 GCB_MOUSE	P01864 mus musculu
13	1100	44.2	322	1 GCB_MOUSE	P01864 mus musculu
14	1087	43.7	330	1 GCB_MOUSE	P01864 mus musculu
15	1080.5	43.4	323	1 GCB_MOUSE	P01864 mus musculu
16	1080.5	43.4	329	1 GCB_MOUSE	P01864 mus musculu
17	1059	42.6	326	1 GCB_MOUSE	P01864 mus musculu
18	1054.5	42.4	327	1 GCB_MOUSE	P01864 mus musculu
19	776.5	31.2	290	1 GCB_MOUSE	P01864 mus musculu
20	478	19.2	454	1 GCB_MOUSE	P01864 mus musculu
21	477.5	19.2	429	1 GCB_MOUSE	P01864 mus musculu
22	474	19.1	421	1 GCB_MOUSE	P01864 mus musculu
23	473	19.0	428	1 GCB_MOUSE	P01864 mus musculu
24	462	18.6	118	1 GCB_MOUSE	P01864 mus musculu
25	457.5	18.4	117	1 GCB_MOUSE	P01864 mus musculu
26	457.5	18.4	117	1 GCB_MOUSE	P01864 mus musculu
27	443.5	17.8	438	1 GCB_MOUSE	P01864 mus musculu
28	436.5	17.6	370	1 GCB_MOUSE	P01864 mus musculu
29	431.5	17.4	438	1 GCB_MOUSE	P01864 mus musculu
30	431	17.3	139	1 GCB_MOUSE	P01864 mus musculu
31	431	17.3	139	1 GCB_MOUSE	P01864 mus musculu
32	430.5	17.3	130	1 GCB_MOUSE	P01864 mus musculu
33	429.5	17.3	136	1 GCB_MOUSE	P01864 mus musculu

## ALIGNMENTS

RESULT	ID	Score	Query Match	Length	ID	Description
1	1	1802	72.5	336	1 GCB_MOUSE	P01866 mus musculu
2	2	1797	72.3	405	1 GCB_MOUSE	P01867 mus musculu
3	3	1419	57.1	330	1 GCAA_MOUSE	P01863 mus musculu
4	4	1414	56.9	399	1 GCAA_MOUSE	P01865 mus musculu
5	5	1385.5	55.7	335	1 GCB_MOUSE	P01864 mus musculu
6	6	1326.5	53.3	333	1 GCB_MOUSE	P01864 mus musculu
7	7	1202.5	48.4	329	1 GCB_MOUSE	P01864 mus musculu
8	8	1170	47.0	329	1 GCB_MOUSE	P01864 mus musculu
9	9	1159	46.6	398	1 GCB_MOUSE	P01864 mus musculu
10	10	1150	46.2	324	1 GCB_MOUSE	P01864 mus musculu
11	11	1145	46.0	393	1 GCB_MOUSE	P01864 mus musculu
12	12	1112	44.7	326	1 GCB_MOUSE	P01864 mus musculu
13	13	1100	44.2	322	1 GCB_MOUSE	P01864 mus musculu
14	14	1087	43.7	330	1 GCB_MOUSE	P01864 mus musculu
15	15	1080.5	43.4	323	1 GCB_MOUSE	P01864 mus musculu
16	16	1080.5	43.4	329	1 GCB_MOUSE	P01864 mus musculu
17	17	1059	42.6	326	1 GCB_MOUSE	P01864 mus musculu
18	18	1054.5	42.4	327	1 GCB_MOUSE	P01864 mus musculu
19	19	776.5	31.2	290	1 GCB_MOUSE	P01864 mus musculu
20	20	478	19.2	454	1 GCB_MOUSE	P01864 mus musculu
21	21	477.5	19.2	429	1 GCB_MOUSE	P01864 mus musculu
22	22	474	19.1	421	1 GCB_MOUSE	P01864 mus musculu
23	23	473	19.0	428	1 GCB_MOUSE	P01864 mus musculu
24	24	462	18.6	118	1 GCB_MOUSE	P01864 mus musculu
25	25	457.5	18.4	117	1 GCB_MOUSE	P01864 mus musculu
26	26	457.5	18.4	117	1 GCB_MOUSE	P01864 mus musculu
27	27	443.5	17.8	438	1 GCB_MOUSE	P01864 mus musculu
28	28	436.5	17.6	370	1 GCB_MOUSE	P01864 mus musculu
29	29	431.5	17.4	438	1 GCB_MOUSE	P01864 mus musculu
30	30	431	17.3	139	1 GCB_MOUSE	P01864 mus musculu
31	31	431	17.3	139	1 GCB_MOUSE	P01864 mus musculu
32	32	430.5	17.3	130	1 GCB_MOUSE	P01864 mus musculu
33	33	429.5	17.3	136	1 GCB_MOUSE	P01864 mus musculu

DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.  
 FT NON\_TER 1  
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).  
 FT DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 118 118 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 150 210 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 256 314  
 FT CARBOHYD 105 105  
 FT MOD\_RES 336 336  
 FT VARIANT 163 163  
 FT VARIANT 194 194  
 FT VARIANT 300 300  
 FT VARIANT 301 301  
 FT CONFLICT 25 25  
 FT CONFLICT 36 36  
 FT CONFLICT 239 239  
 SQ SEQUENCE 336 AA; 3658 MW; 7D879662607C356E CRC64;

Query Match 72.5%; Score 1802; DB 1; Length 336;  
 Best local Similarity 100.0%; Pred. No. 2.8e-118;  
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 119 AKTTPSVYPLAPGCGDTGSSVTLGCLVKGYPRESVYTWNSGLSSSVHTFPALLQSG 178  
 DB 1 AKTTPSVYPLAPGCGDTGSSVTLGCLVKGYPRESVYTWNSGLSSSVHTFPALLQSG 60  
 OY 179 LYTMSVVTPSWTSPQVTCVAVHPASSTVDKLEPSGPISTINPCPCCKCHKCPA 238  
 DB 61 LYTMSVVTPSWTSPQVTCVAVHPASSTVDKLEPSGPISTINPCPCCKCHKCPA 120  
 OY 239 PNEGSPVFIFPPNKKDVLMSLTPKVCVYVDSEDDPDVOISFVNVEVHTAQOT 238  
 DB 121 PNEGSPVFIFPPNKKDVLMSLTPKVCVYVDSEDDPDVOISFVNVEVHTAQOT 180  
 OY 299 HREDYSTRVSTPLIOHODMWSGKEFKCKVNNKDLPSPIERTISKIGLVARPOVYL 358  
 DB 181 HREDYSTRVSTPLIOHODMWSGKEFKCKVNNKDLPSPIERTISKIGLVARPOVYL 240  
 OY 359 PPAEOLSRKDVSLTCLVVGFPNGDISVEWTSNGHTEENYKDPAPVLDSDGSFYISKLN 418  
 DB 241 PPAEOLSRKDVSLTCLVVGFPNGDISVEWTSNGHTEENYKDPAPVLDSDGSFYISKLN 300  
 OY 419 MKTSWEKTDSSFCNVHGLKMYLTKTISRSPEK 454  
 DB 301 MKTSWEKTDSSFCNVHGLKMYLTKTISRSPEK 336  
 RESULT 2  
 GCBM\_MOUSE  
 ID GCBM\_MOUSE STANDARD; PRT; 405 AA.  
 AC P01867;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG GAMA-28 CHAIN C REGION, MEMBRANE-BOUND FORM.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE OF 335-405 FROM N.A.  
 RX MEDLINE=82222190; PubMed=6283537;  
 RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;  
 RT "Nucleotide sequences of gene segments encoding membrane domains of  
 immunoglobulin gamma chains.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).  
 RN [2]  
 RP SEQUENCE OF 335-378 FROM N.A.

RX MEDLINE=82115295; PubMed=6799207;  
 RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,  
 RA Eisenberg D., Wall R.;  
 RT "Gene segments encoding transmembrane carboxyl termini of  
 immunoglobulin gamma chains.";  
 RL Cell 26:19-27(1981).  
 CC -1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA  
 CC SPECIES FOR IG GAMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED  
 CC GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-  
 CC BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED  
 CC IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND  
 CC SEGMENT OF MU CHAINS.  
 CC -1- MISCELLANEOUS: DISULFIDE BONDS BY HOMOLOGY WITH OTHER IG GAMA  
 CC CHAINS.  
 CC -1- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-335 IS ASSUMED TO BE  
 CC IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM.  
 CC -1- MISCELLANEOUS: THE A ALLELE SEQUENCE IS SHOWN.  
 CC -----  
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb.ch/announce/>  
 CC or send an email to [license@isb.slb.ch](mailto:license@isb.slb.ch)).  
 CC -----  
 CC EMBL: J00462; AAB59659.1; ALT\_INIT.  
 DR PIR: C02154; G2MSBM.  
 DR MGD: MG1:96445; Igh-3.  
 DR InterPro: IPR000495; -.  
 DR InterPro: IPR003006; -.  
 DR Pfam: PF00047; Igh-3.  
 DR PROSITE: PS00290; IG\_MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region; Transmembrane;  
 KW Alternative splicing.  
 FT NON\_TER 1  
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).  
 FT DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 118 118 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 150 210  
 FT DISULFID 256 314  
 FT TRANSMEM 352 369  
 FT DOMAIN 370 405  
 SQ SEQUENCE 405 AA; 44330 MW; 89B3CF0A9B6D49FA CRC64;  
 POTENTIAL.  
 CYTOPLASMIC (POTENTIAL).

Query Match 72.3%; Score 1797; DB 1; Length 405;  
 Best local Similarity 100.0%; Pred. No. 8e-118;  
 Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 119 AKTTPSVYPLAPGCGDTGSSVTLGCLVKGYPRESVYTWNSGLSSSVHTFPALLQSG 178  
 DB 1 AKTTPSVYPLAPGCGDTGSSVTLGCLVKGYPRESVYTWNSGLSSSVHTFPALLQSG 60  
 OY 179 LYTMSVVTPSWTSPQVTCVAVHPASSTVDKLEPSGPISTINPCPCCKCHKCPA 238  
 DB 61 LYTMSVVTPSWTSPQVTCVAVHPASSTVDKLEPSGPISTINPCPCCKCHKCPA 120  
 OY 239 PNEGSPVFIFPPNKKDVLMSLTPKVCVYVDSEDDPDVOISFVNVEVHTAQOT 238  
 DB 121 PNEGSPVFIFPPNKKDVLMSLTPKVCVYVDSEDDPDVOISFVNVEVHTAQOT 180  
 OY 299 HREDYSTRVSTPLIOHODMWSGKEFKCKVNNKDLPSPIERTISKIGLVARPOVYL 358  
 DB 181 HREDYSTRVSTPLIOHODMWSGKEFKCKVNNKDLPSPIERTISKIGLVARPOVYL 240  
 OY 359 PPAEOLSRKDVSLTCLVVGFPNGDISVEWTSNGHTEENYKDPAPVLDSDGSFYISKLN 418  
 DB 241 PPAEOLSRKDVSLTCLVVGFPNGDISVEWTSNGHTEENYKDPAPVLDSDGSFYISKLN 300

QY 419 MKTSKEMTDFSCNVHRHGLKNTYKKTISRSPG 453  
D0 301 MKTSKEMTDFSCNVHRHGLKNTYKKTISRSPG 335

RESULT 3  
GCAM\_MOUSE STANDARD; PRT; 330 AA.  
ID GCAM\_MOUSE  
AC P01863;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE 30-MAY-2000 (Rel. 39, Last annotation update)  
DE IG GAMMA-2A CHAIN C REGION, A ALLELE.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81076554; PubMed=6777755;  
RA Sikorav J.-L., Auffray C., Rougeon F.;  
RT "Structure of the constant and 3' untranslated regions of the murine  
RL Nucleic Acids Res. 8:3143-3155(1980).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81198976; PubMed=6262729;  
RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;  
RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene  
RT and evolution of heavy chain genes: further evidence for intervening  
RT sequence-mediated domain transfer.";  
RL Nucleic Acids Res. 9:1365-1381(1981).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=8123894; PubMed=6787604;  
RA Olio R., Auffray C., Morchamps C., Rougeon F.;  
RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes  
RT suggests that exons can be exchanged between genes in a multigenic  
RT family.";  
RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).  
RN [4]  
RP MYELOMA PROTEIN MOPC 173.  
RX MEDLINE=74175517; PubMed=4831970;  
RA Bourgois A., Fougereau M., Rocca-Serra J.;  
RT "Determination of the primary structure of a mouse IgG2a  
RT immunoglobulin: amino-acid sequence of the Fc fragment. Implications  
RT for the evolution of immunoglobulin structure and function.";  
RL Eur. J. Biochem. 43:423-435(1974).  
RN [5]  
RP DISULFIDE BONDS.  
RX MEDLINE=73056887; PubMed=4565406;  
RA de Preval C., Fougereau M.;  
RT "Determination of the primary structure of a mouse gamma 2a  
RT immunoglobulin. Identification of the disulfide bridges.";  
RL Eur. J. Biochem. 30:452-462(1972).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: V00798; CAA24178.1; -  
DR PIR: A02152; G2MSA.  
DR InterPro: IPR000495; -  
DR InterPro: IPR003006; -  
DR Pfam: PF00047; I9; 3.  
DR PROSITE: PS00290; IG\_MHC; 1.  
KW Immunoglobulin domain; Immunoglobulin C region.  
FT NON\_TER 1 1  
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).

FT DISULFID 27 82  
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 144 204  
FT DISULFID 250 308  
FT MOD\_RES 330 330  
SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64; REMOVED POST-TRANSLATIONALLY.

Query Match 57.1%; Score 1419; DB 1; Length 330;  
Best Local Similarity 78.6%; Pred. No. 1.1e-91;  
Matches 264; Conservative 30; Mismatches 36; Indels 6; Gaps 2;

QY 119 AKTTPPSVYPLAPGCGDTGSSVTLGCLVKGIFPESVTVTNSSGSLSSVHTFPALLOGS 178  
D0 1 AKTTPASVYPLAPVCGDGTGSSVTLGCLVKGIFPEPYTLTNSSGSLSSVHTFPALVOSD 60  
179 LYTSSSVTVPSSTWPSOTVCSVAHPASSTVYDKLEPSPGISTINPCPCCKECHKCPA 238  
D0 61 LYTSSSVTVPSSTWPSOTVCSVAHPASSTVYDKLEPSPGISTINPCPCCKECHKCPA 114  
QY 239 PNLGGPSVFTFPPIKIVLMISLTPKVTGVVVDSEDDPVOIISFVNNVEVHTAQTOT 298  
D0 115 PNLGGPSVFTFPPIKIVLMISLTPKVTGVVVDSEDDPVOIISFVNNVEVHTAQTOT 174  
QY 299 HREDYNSTIRVSTLPIODHOMSGKEFKCYVNNKDLPSLERTITSKGLYRAVOYIL 358  
D0 175 HREDYNSTIRVSTLPIODHOMSGKEFKCYVNNKDLPSLERTITSKGLYRAVOYIL 234  
QY 359 PPPAEQSRKQVSLTCLVGVNPGDISVEMTSNGTEENYDTPVLDSDSYFYSLTN 418  
D0 235 PPPAEQSRKQVSLTCLVGVNPGDISVEMTSNGTEENYDTPVLDSDSYFYSLTN 294  
QY 419 MKTSKEMTDFSCNVHRHGLKNTYKKTISRSPG 454  
D0 295 VEKKNWVERNSYSCSVHGLNHHHTTSFSRTPK 330

RESULT 4  
GCAM\_MOUSE STANDARD; PRT; 399 AA.  
ID GCAM\_MOUSE  
AC P01865;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG GAMMA-2A CHAIN C REGION, MEMBRANE-BOUND FORM.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=8222190; PubMed=6283537;  
RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;  
RT "Nucleotide sequences of gene segments encoding membrane domains of  
RT immunoglobulin gamma chains.";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).  
CC -1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA  
CC SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED  
CC GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-  
CC BOUND CHAINS. IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED  
CC IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND  
CC SEGMENT OF MU CHAINS.  
CC -1- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE  
CC IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF  
CC THE A ALLELE.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----

DR EMBL: J00471; AAB59661.1; ALT\_INIT.  
 DR PIR: A02154; G2MSAB.  
 DR MGI: MGI:96443; Igh-1.  
 DR InterPro: IPR000495; -.  
 DR InterPro: IPR003006; -.  
 DR Pfam: PF00047; 19; 3.  
 DR PROSITE: PS00290; IG\_MHC; 1.  
 DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
 KM Transmembrane; Alternative splicing.  
 FT NON\_TER 1 1  
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).  
 FT DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 144 204  
 FT DISULFID 250 308  
 FT TRANSMEM 346 363 POTENTIAL.  
 FT DOMAIN 364 399 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 180 180 N-LINKED (GLUCNA... ) (POTENTIAL).  
 FT SEQUENCE 399 AA; 44020 MM; 4C38138FAD3FF0 CRC64;

Query Match 56.9%; Score 1414; DB 1; Length 399;  
 Best Local Similarity 78.5%; Pred. No. 3, 1e-91;

Matches 263; Conservative 30; Mismatches 36; Indels 6; Gaps 2;

QY 119 AKTTPSVYPLABGCGDTGSSVTLGCLVKGYPESVYTWNSGLSSSVHTFPALLQSG 178  
 1 AKTTASVYPLABGCGDTGSSVTLGCLVKGYPPEVTLTWNSGLSSSVHTFPALLQSD 60  
 DB 179 LYMSSSVYPLABGCGDTGSSVTLGCLVKGYPESVYTWNSGLSSSVHTFPALLQSG 238  
 61 LYTSSSVYPLABGCGDTGSSVTLGCLVKGYPPEVTLTWNSGLSSSVHTFPALLQSD 114  
 DB 239 PNLGGPSVFIIPPNIKDVLMSLTPKVTGVVAVDSEDDPDVQISFVNVNVEHTAQTOT 298  
 115 PNLGGPSVFIIPPNIKDVLMSLTPKVTGVVAVDSEDDPDVQISFVNVNVEHTAQTOT 174  
 DB 299 HRDYNSTRVSTLPDIOHODMMSGKEFKCKVNNKDLPSPIERTISKIGLYRAPQVYIL 358  
 175 HRDYNSTRVSTLPDIOHODMMSGKEFKCKVNNKDLPSPIERTISKIGLYRAPQVYIL 234  
 DB 359 PPAEOLSRKDVSLTGLVYGFNPDISVEMTNSGHTENYKOTAPVLDSDGSYFTSKLN 418  
 235 PPAEOLSRKDVSLTGLVYGFNPDISVEMTNSGHTENYKOTAPVLDSDGSYFTSKLN 294  
 DB 419 MKTSWEKTDSEFCNVRHGLKNYLLKTTISRSPPG 453  
 295 VEKKNVERNISYCSYVHGLNHHHTTKSRTRPG 329

RESULT 5  
 GCAB\_MOUSE STANDARD: PRT; 335 AA.  
 AC P01864;

DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG GAMMA-2A CHAIN C REGION, B ALLELE.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OK NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RA MEDLINE=82037861; PubMed=6170065;  
 RA Schneider P.H., Botwell A.L.M., Mueller-Hill B., Baltimore D.;  
 RT "Multiple differences between the nucleic acid sequences of the

RT IgG2a and IgG2b alleles of the mouse.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).  
 RN [2]

RP SEQUENCE  
 RA MEDLINE=82037777; PubMed=6794027;  
 RA Dognin M.J., Lauwereys M., Strosberg A.D.;  
 RT "Multiple amino acid substitutions between murine gamma 2a heavy  
 chain Fc regions of Ig1a and Ig1b allotypic forms";  
 RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).  
 CC -I- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,  
 FROM BALB/C MICE, AT 158 OF THE POSITIONS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL: J00479; NOT\_ANNOTATED\_CDS.

DR PIR: A02153; G2MSAB.  
 DR InterPro: IPR000495; -.  
 DR InterPro: IPR003006; -.  
 DR Pfam: PF00047; 19; 3.  
 DR PROSITE: PS00290; IG\_MHC; 1.  
 KM Immunoglobulin domain; Immunoglobulin C region.  
 FT NON\_TER 1 1  
 FT SEQUENCE 335 AA; 36596 MM; FA3382792CB13C6 CRC64;

Query Match 55.7%; Score 1385.5; DB 1; Length 335;  
 Best Local Similarity 77.1%; Pred. No. 2, 4e-89;

Matches 259; Conservative 33; Mismatches 43; Indels 1; Gaps 1;

QY 119 AKTTPSVYPLABGCGDTGSSVTLGCLVKGYPESVYTWNSGLSSSVHTFPALLQSG 178  
 1 AKTTASVYPLABGCGDTGSSVTLGCLVKGYPPEVTLTWNSGLSSSVHTFPALLQSG 60  
 DB 179 LYMSSSVYPLABGCGDTGSSVTLGCLVKGYPESVYTWNSGLSSSVHTFPALLQSG 238  
 61 LYTSSSVYPLABGCGDTGSSVTLGCLVKGYPPEVTLTWNSGLSSSVHTFPALLQSD 119  
 DB 239 PNLGGPSVFIIPPNIKDVLMSLTPKVTGVVAVDSEDDPDVQISFVNVNVEHTAQTOT 298  
 120 PNLGGPSVFIIPPNIKDVLMSLTPKVTGVVAVDSEDDPDVQISFVNVNVEHTAQTOT 179  
 DB 299 HRDYNSTRVSTLPDIOHODMMSGKEFKCKVNNKDLPSPIERTISKIGLYRAPQVYIL 358  
 180 HRDYNSTRVSTLPDIOHODMMSGKEFKCKVNNKDLPSPIERTISKIGLYRAPQVYIL 239  
 DB 359 PPAEOLSRKDVSLTGLVYGFNPDISVEMTNSGHTENYKOTAPVLDSDGSYFTSKLN 418  
 240 PPAEOLSRKDVSLTGLVYGFNPDISVEMTNSGHTENYKOTAPVLDSDGSYFTSKLN 299  
 DB 419 MKTSWEKTDSEFCNVRHGLKNYLLKTTISRSPPG 454  
 300 VOKSTWERSLFCASYVHEVLNHHHTTKTISRSLSG 335

RESULT 6  
 GCB\_RAT STANDARD: PRT; 333 AA.  
 ID P20761;

DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG GAMMA-2B CHAIN C REGION.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OK NCBI\_TaxID=10116;  
 RN [1]

Query Match	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps
119 AKTTPSVYPLAPGCGDGTSSVTGCLVKGFPESTVTWNSSGSLSSVHTFPALQSG	53.3%	73.6%	34	50	5	3
1 AQTAPSVYPLAPGCGDGTSSVTGCLVKGFPESTVTWNSSGSLSSVHTFPALQSG						
179 LYTMSSTVTSSTWPSQTVTCVNAHPASSSTTVDKLE-PSGPSTINPCPCCKCHKP						
61 LYTITSSVT--SSFWSPQTVTCVNAHPASSSTTVDKLE-PSGPSTINPCPCCKCHKP						
238 APNLEGGSVTFEPNINIDVLMISLTTPVTCVYVDSEDDPDVQISWVNVNVEHTAQO						
117 VPELLGGSVTFEPNINIDVLMISLTTPVTCVYVDSEDDPDVQISWVNVNVEHTAQO						
298 THREDYNTIRVSTPLPQHDMDMSGKFEKCKVNNKDLPSPIERTISIKIGLVRAPOYII						
177 PREEDYNTIRVSTPLPQHDMDMSGKFEKCKVNNKDLPSPIERTISIKIGLVRAPOYII						
358 LPPAEOISRKVDLSLTCLVGFNPNPDISVEMTNSGHTENTKDTAPVLDSGSEYFIYSKL						
237 MGPPTEQLTEQVLSLTCLVGFNPNPDISVEMTNSGHTENTKDTAPVLDSGSEYFIYSKL						
418 NMKTSKMEKTDSEFCNVNHEGLKNTYLLKTKTISRSFGK						
297 NVERSRMDSRAPFVCSVYVHEGLNHNHVEKSSISRPCK						
SEQUENCE FROM N.A.						
Brieglebmann M.;						
"Evolution of the rat immunoglobulin gamma heavy-chain gene family."						
Gene 74:473-482(1988).						
PIR: PS0018; PS0018						
InterPro: IPR000495; -						
InterPro: IPR003006; -						
Pfam: PF00047; 1g; 3.						
PROSITE: PS00290; IG_MHC; 1.						
Immunoglobulin domain; Immunoglobulin C region.						
NON_TER						
DISULFID	15	15				
DISULFID	27	80				
DISULFID	106	106				
DISULFID	109	109				
DISULFID	112	112				
DISULFID	115	115				
DISULFID	147	207				
DISULFID	253	311				
SEQUENCE	333 AA;	36497 MW;	55F8B64D48D460A6	CRC64;		

CC		between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC		the European Bioinformatics Institute. There are no restrictions on its
CC		use by non-profit institutions as long as its content is in no way
CC		modified and this statement is not removed. Usage by and for commercial
CC		entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>
CC		or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC		-----
DR	EMBL; X07189; CAA30169.1; -.	
DR	PIR; S00847; S00847.	
DR	InterPro; IPR000495; -.	
DR	InterPro; IPR003006; -.	
DR	Pfam; PF00047; 1g; 3.	
DR	PROSITE; PS00290; IG_MHC; 1.	
KW	Immunoglobulin domain; Immunoglobulin C region.	
FT	NON_TER 1 1	
FT	DOMAIN 1 97	CH1.
FT	DOMAIN 98 113	HINGE.
FT	DOMAIN 114 222	CH2.
FT	DOMAIN 223 329	CH3.
FT	DISULFID 15 15	INTERCHAIN (WITH A LIGHT CHAIN).
FT	DISULFID 27 82	
FT	DISULFID 111 111	INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 113 113	INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 143 203	
FT	DISULFID 249 307	
SQ	SEQUENCE 329 AA; 36571 MW; 5FCDD7B7933850773 CRC64;	

Query Match	Similarity	48.4%	Score 1202.5	DB 1	Length 329
Best Local	Conservative	68.2%	Pred. No. 1.2e-76	Mismatches 35	Indels 7
Matches 229	Conservative	65	Mismatches 65	Indels 7	Gaps 4
OY	119	AKTTPSVYPLAPGCGDGTSSVTLTGCLVKGFPEPSVVTWNMSSGLSSSVHTFPALLQSG	178	1	ARTAPSVYPLVPGSGSGISGSLVTLTGCLVKGFPEPSVVTWNMSSGLSSGVHTFPALLQSG
DB	1	ARTAPSVYPLVPGSGSGISGSLVTLTGCLVKGFPEPSVVTWNMSSGLSSGVHTFPALLQSG	60		
OY	179	LYTMSSSVTVPSSTMPSSQTVTCVAHPASSSTTVDKLEBSPGISTINCPQCKECHKCPA	238		
DB	61	LYTSSSVTVPSSTMPSSQTVTCVAHPASSSTTVDKLEBSPGISTINCPQCKECHKCPA	114		
OY	239	PVLEGGPSVFIEPPINIKIVMLMTSPKTYCVYVDSEDDPDVQISFNNVNVHTHATQOT	298		
DB	115	DNL-GRPSTFIEPPINIKIVMLMTSPKTYCVYVDSEDDPDVQISFNNVNVHTHATQOT	173		
OY	299	HREDYNSTIRVSTLPIQHODMMSGKEFKCKYNNKDLPSLERTISKIKGLVADQVYL	358		
DB	174	HEEOQNGTFRRVYSTLIHOHODMMSGKEFKCKYNNKDLPSLERTISKIKGLVADQVYL	233		
OY	359	PPAPQSLRKQVSLCLVVGFGNDGISVEMTNSNGHTENYKDTAVLSDGSFYFLSKLN	418		
DB	234	PPPRQMSKNKSLCLVVGFGNDGISVEMTNSNGHTENYKDTAVLSDGSFYFLSKLN	293		
OY	419	MKTSKMEKTDSPSCNVHRHGLKNLYLAKTTISRPCK	454		
DB	294	VDTDSMNRGDIYTCGVHVALHNNHTQKNLSRPSK	329		
RESULT	8				
GC3_MOUSE	STANDARD	PRT	329 AA		
ID	GC3_MOUSE	P22436			
AC		01-AUG-1991	(Rel. 19, Created)		
DT		01-AUG-1991	(Rel. 19, Last sequence update)		
DT		15-JUL-1999	(Rel. 38, Last annotation update)		
DE		IG GAMMA-3 CHAIN C REGION	SECRETED FORM.		
OS		Mus musculus	(Mouse)		
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC		Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.			
OX		NCBI_TaxID=10090;			
RN		[1]			
RP		SEQUENCE FROM N.A.			
RP		MEDLINE=85027161; PubMed=6092053;			
RA		Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,			

RA Tucker P.W., Blattner F.R.;  
RT "Structural analysis of the murine IgG3 constant region gene."  
RL EMBO J. 3:2041-2046(1984).  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: J00451; NOT\_ANNOTATED\_CDS.  
CC PIR: B02156; G3MSC.  
CC InterPro: IPR000495; -  
CC InterPro: IPR003006; -  
CC Pfam: PF00047; 1g; 3.  
CC PROSITE: PS00290; IG\_MHC.1.  
CC Immunoglobulin C region; Glycoprotein; Transmembrane;  
CC Alternative splicing.  
CC NON\_TER 1 97 CH1.  
CC DOMAIN 98 113 HINGE.  
CC DOMAIN 114 223 CH2.  
CC DOMAIN 224 327 CH3.  
CC DOMAIN 328 362 CH4.  
CC SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;  
CC -----  
Query Match 47.0%; Score 1170; DB 1; Length 329;  
Best Local Similarity 66.2%; Pred. No. 2.1e-74;  
Matches 221; Conservative 33; Mismatches 74; Indels 6; Gaps 1;  
QY 121 TTPSYVPLAPCGDGTGSSVTGCLVKGFPESTVVTNMGSLSSVHTFPALLQSGLY 180  
DB 2 TTPSYVPLAPCGDGTGSSVTGCLVKGFPESTVVTNMGSLSSVHTFPALLQSGLY 61  
QY 181 TMSSTVTPSSWTPSQVTGCSVAHPASSTVDKLEPSPGISTINPCPCCKCHKCPAPN 240  
DB 62 SLSSLYTVSSWTPSQVTGCSVAHPASSTVDKLEPSPGISTINPCPCCKCHKCPAPN 115  
QY 241 LBGSPVFLFPPIKIVLMISLTPKVTGVVVDSEDDPVQISWFWNNVHTAQTQTHR 300  
DB 116 ILGSPVFLFPPIKIVLMISLTPKVTGVVVDSEDDPVQISWFWNNVHTAQTQTHR 175  
QY 301 EDYNTIRVSTLPLOHODMMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPOVYILPP 360  
DB 176 AOVNSTFRVVSALPIOHODMMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPOVYILPP 235  
QY 361 PAEOLSRKDVSLTCLVVGFPDGSIVEMTNGHTEENYKDTAPVLDSDGSYFIYSKLNK 420  
DB 236 PREOMSKKRVSLTCLVVGFPDGSIVEMTNGHTEENYKDTAPVLDSDGSYFIYSKLNK 295  
QY 421 TSKWEKTDSCNVHREGIKNYLTKTISRSPK 454  
DB 296 TDSWLGELFTCSVYVHALLNHHHTOKNLSRSPK 329  
CC -----  
RESULT 9  
GC3M\_MOUSE STANDARD; PRT; 398 AA.  
AC P03987;  
DT 23-OCT-1986 (Rel. 02, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG GAMMA-3 CHAIN C REGION, MEMBRANE-BOUND FORM.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85027161; PubMed=6092053;  
RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,

RA Tucker P.W., Blattner F.R.;  
RT "Structural analysis of the murine IgG3 constant region gene."  
RL EMBO J. 3:2041-2046(1984).  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: J00451; AAB59655.1; ALT\_SEQ.  
CC PIR: A02156; G3MSC.  
CC InterPro: IPR000495; -  
CC InterPro: IPR003006; -  
CC Pfam: PF00047; 1g; 3.  
CC PROSITE: PS00290; IG\_MHC.1.  
CC Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
CC Transmembrane; Alternative splicing.  
CC NON\_TER 1 97 CH1.  
CC DOMAIN 98 113 HINGE.  
CC DOMAIN 114 223 CH2.  
CC DOMAIN 224 327 CH3.  
CC TRANSMEM 346 362 POTENTIAL.  
CC DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).  
CC CONFLICT 342 342 E -> G (IN REF. 2).  
CC CONFLICT 388 388 E -> Q (IN REF. 2).  
CC SEQUENCE 398 AA; 43929 MW; C7F264B50A41B95 CRC64;  
CC -----  
Query Match 46.6%; Score 1159; DB 1; Length 398;  
Best Local Similarity 66.0%; Pred. No. 1.6e-73;  
Matches 219; Conservative 33; Mismatches 74; Indels 6; Gaps 1;  
QY 121 TTPSYVPLAPCGDGTGSSVTGCLVKGFPESTVVTNMGSLSSVHTFPALLQSGLY 180  
DB 2 TTPSYVPLAPCGDGTGSSVTGCLVKGFPESTVVTNMGSLSSVHTFPALLQSGLY 61  
QY 181 TMSSTVTPSSWTPSQVTGCSVAHPASSTVDKLEPSPGISTINPCPCCKCHKCPAPN 240  
DB 62 SLSSLYTVSSWTPSQVTGCSVAHPASSTVDKLEPSPGISTINPCPCCKCHKCPAPN 115  
QY 241 LBGSPVFLFPPIKIVLMISLTPKVTGVVVDSEDDPVQISWFWNNVHTAQTQTHR 300  
DB 116 ILGSPVFLFPPIKIVLMISLTPKVTGVVVDSEDDPVQISWFWNNVHTAQTQTHR 175  
QY 301 EDYNTIRVSTLPLOHODMMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPOVYILPP 360  
DB 176 AOVNSTFRVVSALPIOHODMMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPOVYILPP 235  
QY 361 PAEOLSRKDVSLTCLVVGFPDGSIVEMTNGHTEENYKDTAPVLDSDGSYFIYSKLNK 420  
DB 236 PREOMSKKRVSLTCLVVGFPDGSIVEMTNGHTEENYKDTAPVLDSDGSYFIYSKLNK 295  
QY 421 TSKWEKTDSCNVHREGIKNYLTKTISRSP 452  
DB 296 TDSWLGELFTCSVYVHALLNHHHTOKNLSRSP 327  
CC -----  
RESULT 10  
GC1\_MOUSE

ID GC1\_MOUSE STANDARD; PRT; 324 AA.  
 AC P01869;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE IG GAMMA-1 CHAIN C REGION.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Honjo T., Ohta M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,  
 RA Takahashi N., Mano Y.;  
 RT "Cloning and complete nucleotide sequence of mouse immunoglobulin  
 RT gamma 1 chain gene.";  
 RL Cell 18:559-568(1979).  
 RN [2]  
 RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).  
 RX MEDLINE=80202559; Pubmed=6769752;  
 RA Ohta M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,  
 RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;  
 RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences  
 RT cloned in a bacterial plasmid.";  
 RL Gene 9:87-97(1980).  
 RN [3]  
 RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).  
 RX MEDLINE=80012837; Pubmed=113776;  
 RA Rogers J., Clarke P., Salsner W.;  
 RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin  
 RT heavy chain.";  
 RL Nucleic Acids Res. 6:3305-3321(1979).  
 RN [4]  
 RP SEQUENCE (MYELOMA PROTEIN MOPC 21).  
 RX MEDLINE=78242288; Pubmed=98524;  
 RA Aetugbo K.;  
 RT "Evolution of immunoglobulin subclasses. Primary structure of a  
 RT murine myeloma gamma1 chain.";  
 RL J. Biol. Chem. 253:6068-6075(1978).  
 RN [5]  
 RP DISULFIDE BONDS (MOPC 21).  
 RX MEDLINE=73008889; Pubmed=5073237;  
 RA Swasti J., Milstein C.;  
 RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";  
 RL Biochem. J. 126:837-850(1972).  
 CC -----  
 CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC  
 DR EMBL: V00793; CAA24172.1; -;  
 DR EMBL: V00793; CAA24173.1; -;  
 DR EMBL: V00793; CAA24174.1; -;  
 DR EMBL: V00793; CAA24175.1; -;  
 DR EMBL: V00795; CAA24176.1; -;  
 DR PIR: A02159; G1MS  
 DR Glycosited3; P01868; -;  
 DR MGD: MG196446; 19n-4.  
 DR InterPro: IPR000495; -;  
 DR InterPro: IPR003006; -;  
 DR Pfam: PF00047; 19; 3.  
 DR PROSITE: PS00290; IG\_MHC; 1.  
 KM Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
 KW Alternative splicing.  
 FT NON\_TER 1 97 CH1.  
 FT DOMAIN 98 110 HINGE.  
 FT DOMAIN 111 217 CH2.

FT DOMAIN 218 324 CH3.  
 FT DISULFID 27 82  
 FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).  
 FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 138 198  
 FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).  
 FT DISULFID 244 302  
 FT MOD\_RES 324 324  
 FT CONFLICT 276 276 N -> D (IN REF. 3).  
 FT CONFLICT 278 278 N -> D (IN REF. 3).  
 SQ SEQUENCE 324 AA; 35704 MW; A338812E3D1EF2C93 CRC64;  
  
 Query Match 46.28; Score 1150; DB 1; Length 324;  
 Best Local Similarity 64.6%; Pred. No. 5.2e-73;  
 Matches 217; Conservative 45; Mismatches 62; Indels 12; Gaps 4;  
  
 QY 119 AKTPPSVYPLAPCGDPTGSSVTLGCLVKGYPFESVYVYNNSSLSSTVTFPALLQSG 178  
 DB 1 AKTPPSVYPLAPGSAATNSMTVLGCLVKGYPFVTVNNSGSLSSGVTFPAVLQSD 60  
 QY 179 LYTSSSVTVPSSTWPSOTVTCVAHPASSSTVTKLEPSSGPSTINPCPCCKCHKCPA 238  
 DB 61 LYTSSSVTVPSSTWPSOTVTCVAHPASSSTVTKLEPSSGPSTINPCPCCKCHKCPA 238  
 QY 239 PNEGSPSVFLFPNIDVLMISLTPKVCVVDVSDPDVQISMFVNVVHTAQTQT 298  
 DB 112 PEVS---SVFLFPKPKVDVLTITLTPKVCVVDVSDPDVQISMFVNVVHTAQTQT 168  
 QY 299 HREDYNTIRVSTLPIQHDMMGKREKCVNNKDLPSPIERTISKIQLVRAPOVYIL 358  
 DB 169 REQFNSTFRSVSELPIMHODMLNGKREKCVNNKDLPSPIERTISKIQLVRAPOVYIL 228  
 QY 359 PPPEAOLSRKVSSTLCVYVGNPDIVSWETSNGHTEENYDTPAVLSDSSTYFYSKLN 418  
 DB 229 PPPEAOLSRKVSSTLCVYVGNPDIVSWETSNGHTEENYDTPAVLSDSSTYFYSKLN 288  
 QY 419 MKTSKWEKTDSPSCNVRHEGLKNTYLLKRTISRSPPGK 454  
 DB 289 VQKSNWEAGNFTSCVYLHEGLNHTKESLSHSPGK 324  
  
 RESULT 11  
 GC1\_MOUSE STANDARD; PRT; 393 AA.  
 ID GC1\_MOUSE  
 AC P01869;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE IG GAMMA-1 CHAIN C REGION. MEMBRANE-BOUND FORM.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Honjo T., Ohta M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,  
 RA Takahashi N., Mano Y.;  
 RT "Cloning and complete nucleotide sequence of mouse immunoglobulin  
 RT gamma 1 chain gene.";  
 RL Cell 18:559-568(1979).  
 RN [2]  
 RP SEQUENCE OF 323-393 FROM N.A.  
 RX MEDLINE=82197626; Pubmed=6804950;  
 RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;  
 RT "mRNA for surface immunoglobulin gamma chains encodes a highly  
 RT conserved transmembrane sequence and a 28-residue intracellular  
 RT domain.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).  
 RN [3]

RP SEQUENCE OF 323-366 FROM N.A.  
 RA MEDLINE=82115295; PubMed=6799207;  
 RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Knehl M.,  
 RA Eisenberg D., Wall R.;  
 RT "Gene segments encoding transmembrane carboxyl termini of  
 RT immunoglobulin gamma chains.";  
 RL Cell 26:19-27(1981).  
 RN  
 RP SEQUENCE OF 1-44 FROM N.A.  
 RX MEDLINE=82222190; PubMed=6283537;  
 RX Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;  
 RT "Nucleotide sequences of gene segments encoding membrane domains of  
 RT immunoglobulin gamma chains.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).  
 CC -I- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA  
 CC SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED  
 CC GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-  
 CC BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED  
 CC IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND  
 CC SEGMENT OF MU CHAINS.  
 -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 -----  
 CC  
 DR EMBL: V00793; CAA24172.1;  
 DR EMBL: V00793; CAA24173.1;  
 DR EMBL: V00793; CAA24174.1;  
 DR PIR: B02159; GIMSM.  
 DR MGD: MGI:96446; Igh-4.  
 DR InterPro: IPR000495;  
 DR InterPro: IPR003006;  
 DR Pfam: PF00047; 19; 3.  
 DR PROSITE: PS00290; IG\_MHC; 1.  
 DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
 KW Alternative splicing; Transmembrane.  
 FT NON\_TER 1 1  
 FT DOMAIN 1 97 CH1.  
 FT DOMAIN 98 110 HINGE.  
 FT DOMAIN 111 217 HINGE.  
 FT DISULFID 218 324 CH3.  
 FT DISULFID 27 82  
 FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).  
 FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 138 198 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT CARBOHYD 174 174  
 FT DISULFID 244 302  
 FT TRANSMEM 340 357  
 FT DOMAIN 358 393  
 FT SEQUENCE 393 AA; 43386 MW; 4CC8343B7A1CE27 CRC64;  
 SO  
 Query Match 46.0%; Score 1145; DB 1; Length 393;  
 Best Local Similarity 64.5%; Pred. No. 1.5e-72;  
 Matches 216; Conservative 45; Mismatches 62; Indels 12; Gaps 4;  
 QY 119 AKTTPSVPLAPGCGDITGSSVTLGCLVKGYPPEVYTNWNSGSLSSVHFPALQSG 178  
 DB 1 AKTTPSVPLAPGSAQNSMTLGLVKGYPPEVYTNWNSGSLSSVHFPALQSD 60  
 QY 179 LYTMSSTVVPSPSTWPSQVTCVAHPASTVYDKLEBSPGISTINPCPKCKEHCPCA 238  
 DB 61 LYTLLSSVVPSPSPSEVITCVNAHPASTKYDKKIYV-----RDC-GCKPC-ICTIV 111  
 QY 239 PULEGSPVFIFPPNKKVLMISLTPKVCVVDVSEDDPDVQISFVNNAVETHAQOT 298  
 DB 112 PEVS---SVFIFPPKPKVDLITLTPKVCVVDVSKDDPEVQSFVVDVEVHTAQT 168

QY 299 HREDYNSTRVSTLPIQHDWMSGKEFKCKYNNKDLSPRIERTISKIGLVAPOVYTL 358  
 DB 169 REQGFNSTFRSVSELPIMQDNLNGKEFKCRVNSAFAPIETISKIGRPARPVYTI 228  
 QY 359 PPEAQLSKRDVSLTGLVGFNPDISVEMTSGNTEENYKDTAPVLDSDGYEYSKIN 418  
 DB 229 PPKPEQMAKDQVSLTCMINDPEPDIETVEQWQPAENYKNTQPIYNTNGSYFYVSKLN 288  
 QY 419 MKTSKEKTDSPSCNVRHGLKNYIKKTIISRSPG 453  
 DB 289 VQKSNMEAGNTFTCSVLHGLHNNHTEKLSHSPG 323  
 RESULT 12  
 ID GCL\_RAT STANDARD; PRT; 326 AA.  
 AC P20759;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG GAMMA-1 CHAIN C REGION.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=89232738; PubMed=3149946;  
 RX Brueggemann M.;  
 RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";  
 RL Gene 74:473-482(1988).  
 DR PIR: PS0017; PS0017.  
 DR InterPro: IPR000495;  
 DR InterPro: IPR003006;  
 DR Pfam: PF00047; 19; 3.  
 DR PROSITE: PS00290; IG\_MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.  
 FT NON\_TER 1 1  
 FT DOMAIN 1 97 CH1.  
 FT DOMAIN 98 112 HINGE.  
 FT DOMAIN 113 219 HINGE.  
 FT DOMAIN 220 326 CH3.  
 FT DISULFID 27 82  
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 140 200  
 FT DISULFID 246 304  
 FT CARBOHYD 176 176  
 FT SEQUENCE 326 AA; 35946 MW; 013BAB45E49B9DA CRC64;  
 SO  
 Query Match 44.7%; Score 1112; DB 1; Length 326;  
 Best Local Similarity 61.9%; Pred. No. 2.3e-70;  
 Matches 208; Conservative 50; Mismatches 68; Indels 10; Gaps 3;  
 QY 119 AKTTPSVPLAPGCGDITGSSVTLGCLVKGYPPEVYTNWNSGSLSSVHFPALQSG 178  
 DB 1 AKTTPSVPLAPGALKNSMTLGLVKGYPPEVYTNWNSGSLSSVHFPALQSG 60  
 QY 179 LYTMSSTVVPSPSTWPSQVTCVAHPASTVYDKLEBSPGISTINPCPKCKEHCPCA 238  
 DB 61 LYTLLSSVVPSPSTWPSQVITCVNAHPASTVYDKKIYV-----NCGGDKPC-ICTIG 113  
 QY 239 PULEGSPVFIFPPNKKVLMISLTPKVCVVDVSEDDPDVQISFVNNAVETHAQOT 298  
 DB 114 SEVS---SVFIFPPKPKVDLITLTPKVCVVDVSDQDEVEHFSFVVDVEVHTAQT 170  
 QY 299 HREDYNSTRVSTLPIQHDWMSGKEFKCKYNNKDLSPRIERTISKIGLVAPOVYTL 358  
 DB 171 PEOFNSTFRSVSELPILHQDNLNGRTFRCKVTSAAFPSPIEKTSKPGRQVPHVYTM 230



[illegible]

RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.".   
 RL Gene 74:473-482(1988).   
 CC -----   
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration   
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -   
 CC the European Bioinformatics Institute. There are no restrictions on ways   
 CC use by non-profit institutions as long as its content is in no way   
 CC modified and this statement is not removed. Usage by and for commercial   
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>   
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).   
 CC -----

DR	EMBL; M13604: AAAA1376.1; ALT_INIT.
DR	PIR; PS0019; PS0019.
DR	InterPro; IPR000495; -
DR	InterPro; IPR003006; -
DR	Pfam; PF00047; Ig; 2.
DR	PROSITE; PS00290; IG_MHC; 1.
KW	Immunoglobulin domain; Immunoglobulin C region.
FT	NON_TER 1
FT	DISULFID 27 82
FT	DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 136 196
FT	DISULFID 242 300
FT	CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE 322 AA; 35186 MW; EE6A136A9DE01EDB CRC64;

[illegible]

RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).

KA MEDLINE#11064024; PubMed#2483771;  
 RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,  
 RA Maxdal M.J., Edelman G.M.;  
 RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino  
 RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4".  
 RL Biochemistry 9:3161-3170(1970).  
 [3]  
 RN SEQUENCE OF 136-329 (EU).  
 RP MEDLINE#71064025; PubMed#5530842;  
 RX Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,  
 RA Edelman G.M.;  
 RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino  
 RT acid sequence of heavy-chain cyanogen bromide fragments H5-H7".  
 RL Biochemistry 9:3171-3181(1970).

KN [4]  
RP SEQUENCE (MYELOMA PROTEIN NIE).  
RX MEDLINE=77070269; PubMed=826475;  
RA Postingsl H., Hilschmann N.;  
RT "The rule of antibody structure. The primary structure of a  
RT monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The  
RT chymotryptic peptides of the H-chain, alignment of the tryptic  
RT peptides and discussion of the complete structure.;"  
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).

KN (13)  
RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.  
RX MEDLINE-63268131; Pubmed-6884994.  
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.:  
RT "three-dimensional structure determination of antibodies. Primary  
RL structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.",  
Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1963).

RN  
RP  
RQ  
RX  
RY  
RA  
RB  
RC  
RD  
RE  
RF  
RG  
RH  
RI  
RJ  
RK  
RL

101  
DISULFIDE BONDS.  
MEDLINE=71064027; PubMed=4923144;  
Gall W.E., Edelman G.M.;  
"The covalent structure of a human gamma G-immunoglobulin. X  
Intrachain disulfide bonds.";  
Biochemistry 9:3188-3196(1970).

RN 1/1  
RP DISULFIDE BONDS.  
RX MEDLINE=77070267; PubMed=1002129;  
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.:

RT "Rule of antibody structure. The primary structure of a monoclonal  
 RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and  
 RT characterization of the protein, the L- and H-chains, the  
 RT cyanogen bromide cleavage products, and the disulfide bridges."  
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
 RX MEDLINE-81208100; PubMed-7236608;  
 RA Deisenhofer J.:  
 RT "Crystallographic refinement and atomic models of a human Fc fragment  
 RT and its complex with fragment B of protein A from *Staphylococcus*  
 RT aureus at 2.9- and 2.8-A resolution."  
 RL Biochemistry 20:2361-2370(1981).  
 CC -I- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-R, & THE  
 CC GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3)  
 CC MARKER & THE GIM (NON-1) MARKERS.  
 CC -I- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF  
 CC 35, 116, 198, 269 & 272  
 CC -I- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES  
 CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES  
 CC 268-272.  
 CC -I- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF  
 CC RESIDUES 198, 267&272.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: J00228; AAC82527.1; ALT\_INIT.  
 DR PIR: A02146; GHU.  
 DR PDB: 1RC1; 15-JUL-92.  
 DR PDB: 1RC2; 15-JUL-92.  
 DR MIM: 147100;  
 DR InterPro: IPR000495; -  
 DR InterPro: IPR003006; -  
 DR Pfam: PF00047; 1g; 3.  
 DR PROSITE: PS00290; IG\_MHC; 2.  
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
 KW 3D-structure.  
 FT NON\_TER 1 98  
 FT DOMAIN 99 110 CH1.  
 FT DOMAIN 111 123 HINGE.  
 FT DOMAIN 224 330 CH2.  
 FT DISULFID 27 83 CH3.  
 FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).  
 FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).  
 FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).  
 FT DISULFID 144 204 INTERCHAIN (WITH HEAVY CHAIN).  
 FT DISULFID 250 308  
 FT CARBOHYD 180 180  
 FT MOD\_RES 330 330  
 FT VARIANT 97 97  
 FT VARIANT 239 239  
 FT VARIANT 241 241  
 FT STRAND 123 126  
 FT HELIX 130 134  
 FT TURN 136 137  
 FT STRAND 141 148  
 FT TURN 158 162  
 FT STRAND 163 164  
 FT STRAND 175 178  
 FT STRAND 183 190  
 FT HELIX 193 197  
 FT TURN 198 199  
 FT TURN 198 199

FT STRAND 202 206  
 FT STRAND 215 219  
 FT STRAND 227 227  
 FT STRAND 230 234  
 FT HELIX 238 240  
 FT TURN 241 242  
 FT STRAND 245 256  
 FT STRAND 260 266  
 FT TURN 267 268  
 FT STRAND 269 270  
 FT STRAND 274 276  
 FT STRAND 280 281  
 FT TURN 283 284  
 FT STRAND 287 296  
 FT HELIX 297 301  
 FT TURN 302 303  
 FT STRAND 306 312  
 FT TURN 313 314  
 FT TURN 316 317  
 FT STRAND 320 324  
 SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA3D CRC64;  
  
 Query Match 43.7%; Score 1087; DB 1; Length 330;  
 Best Local Similarity 60.8%; Pred. No. 1.3e-68;  
 Matches 205; Conservative 49; Mismatches 75; Indels 8; Gaps 3;  
  
 QY 119 AKTTPSVYPLAPGCGDDTGGSVTLGCLVKGFPESVTWNMNSGLSSVHTFPALLO-S 177  
 DB 1 ASKGGSVFPLAPSSKSTGGTALCLVKNDFPEVYVSMNSGALTSVHTFPALVSS 60  
 QY 178 GLYTMSSVTVPSSTWPSQVTCVAHPASSSTVDKLEPSPGISTINPCPKCKHCP 237  
 DB 61 GLYLSSTVTVPSSSLGDTQYICNVNHRKPSNTRKVDKVEPKSCDKT-HRCP-----CP 113  
 QY 238 APNLEGGPSVFIFPPNIRKIVLMISLTPKVTQYVVDVSEDDPDVQISMFPNNVEYHTAQ 297  
 DB 114 APDLGGPSVFIFPPNIRKIVLMISLTPKVTQYVVDVSEDDPDVQISMFPNNVEYHTAQ 173  
 QY 298 THREYNTSTIRYVSTPIOHODMMSGKFEKCYNNKDLPSPIERTSKIKGLVRAPOYI 357  
 DB 174 PREQYNSTIRYVSVLTIVYHODMLNKEKCYNNKDLPSPIERTSKIKGLVRAPOYI 233  
 QY 358 LPPPAQLSRKDVSLTCLVYGFNPGDISEWTSNGHTEENYKDTAVLDSDGSYFLYSKL 417  
 DB 234 LPPSRDELTKFKNVSLTCLVKGFPYSDIAVEMESNGPENNYKDTAVLDSDGSYFLYSKL 293  
 QY 418 NAKTSKTEKTDSPSCNVRHREGIKNYLAKTISRSPCK 454  
 DB 294 TVDKSRMOQGNVSCSVMHDLNHYTOKSLSPCK 330  
  
 RESULT 15  
 GC\_RABIT STANDARD; PRT; 323 AA.  
 AC P01870;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG GAMMA CHAIN C REGION.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxId=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-84030930; PubMed-6313520;  
 RX Bernstein K.E., Alexander C.B., Mage R.G.;  
 RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant  
 RL F-1 haplotype."  
 RL Immunogenetics 18:387-397(1983).  
 RN [2]  
 RP SEQUENCE OF 1-128.

RX MEDLINE=76135469; PubMed=1243651;  
 RA Pratt D.M., Mole L.E.;  
 RT "Sequence studies on the constant region of the Fd sections of rabbit  
 immunoglobulin G of different allotype.";  
 RL Biochem. J. 151:337-349(1975).  
 RN [3]  
 RP SEQUENCE OF 88-266 FROM N.A.  
 RX MEDLINE=83299917; PubMed=6193512;  
 RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;  
 RT "Heavy chain genes of rabbit IgG: Isolation of a cDNA encoding gamma  
 heavy chain and identification of two genomic C gamma genes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).  
 RN [4]  
 RP SEQUENCE OF 132-161.  
 RX MEDLINE=70110015; PubMed=5461106;  
 RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;  
 RT "Sequence studies of the Fd section of the heavy chain of rabbit  
 immunoglobulin G.";  
 RL Biochem. J. 116:249-259(1970).  
 RN [5]  
 RP SEQUENCE OF 129-131 AND 155-322.  
 RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;  
 RL (in) Killander J. (eds.);  
 RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,  
 Stockholm (1967).  
 CC CC  
 CC -1- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,  
 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15  
 MARKERS AND REF.5 THE E15 MARKER.  
 CC CC  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC CC  
 CC EMBL: M16426; AAA31289.1; -.  
 DR PIR: A02161; GHRB.  
 DR InterPro: IPR000495; -.  
 DR InterPro: IPR003006; -.  
 DR Pfam: PF00047; 19; 3.  
 DR PROSITE: PS00290; IG\_MHC; 1.  
 KM Immunoglobulin domain; Immunoglobulin C region.  
 FT NON\_TER 1 1  
 FT VARIANT 104 104 T -> M (IN D11 MARKER).  
 FT VARIANT 185 185 T -> A (IN E15 MARKER).  
 FT CONFLICT 48 48 N -> E (IN REF. 2).  
 FT CONFLICT 71 71 V -> VPV (IN REF. 2).  
 FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).  
 FT CONFLICT 173 173 N -> D (IN REF. 5).  
 FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).  
 FT CONFLICT 201 201 N -> D (IN REF. 5).  
 FT CONFLICT 218 218 O -> E (IN REF. 5).  
 FT CONFLICT 233 233 E -> Q (IN REF. 5).  
 FT CONFLICT 246 246 N -> D (IN REF. 5).  
 FT CONFLICT 256 256 E -> G (IN REF. 5).  
 FT CONFLICT 260 260 N -> D (IN REF. 5).  
 FT CONFLICT 266 266 N -> D (IN REF. 5).  
 FT CONFLICT 280 280 Y -> W (IN REF. 5).  
 FT CONFLICT 284 284 N -> S (IN REF. 5).  
 SQ SEQUENCE 323 AA; 35404 MW; 69EBAA118D579A8B CRC64;

Query Match 43.4%; Score 1080.5; DB 1; Length 323;  
 Best Local Similarity 61.4%; Pred. No. 3.4e-68;  
 Matches 205; Conservative 48; Mismatches 62; Indels 19; Gaps 4;

QY 124 PSYPLAPGCCDITGSSYTLGLVKGIFPESVYTWNSGSLSSSVHFPALIQ-SGLYTM 182  
 DB 6 PSYPLAPGCCDITGSSYTLGLVKGIFPESVYTWNSGSLSSSVHFPALIQ-SGLYTM 182  
 QY 183 SSSVTVSSSTWPSQTVCSVAHNPASSSTTVDKLKPSPGISINPCPKCECHK--CPAPN 240

DB 66 SSVSVTVSS--SQPYTCNVAHNPALNTRKVDKTVAPS-----TCSKPTCPEPE 109  
 QY 241 LEGGSPVFIFPPPKIKDVMISLTPRYTCVVVDVSEDDPDVOISFVNNEVHTAQTOTHR 300  
 DB 110 LLGGSPVFIFPPPKPKDMLISRTPEVTCVVVDVSDPDPEVQFTWYINNEQVTRAPPLRE 169  
 QY 301 EDVNSTTRVSTLPLTHODDMSGKEFKCKVNNKPLSPRIERTISKINGLVRAPOVYILPP 360  
 DB 170 QQFNSTIRVSTLPLTHODDMLRGEFKCKVNNKLPAPITERTISKARQPLEPVYITWGP 229  
 QY 361 PAEOLSRKDVSLTCLVYGFNPGDISVEWTSNGHTEENKOTAPYLDSDGSYFIYSKIMK 420  
 DB 230 PREELSSRSVSLTCMINGFYPSDISVEWENKGAEDNKTTTPAYLDSGSIYFLNKLSPV 289  
 QY 421 TSKWEKTDVFSQCNVRHEGLKNVYLKTTISRSPGK 454  
 DB 290 TSEWQRGDVPFCSVMEHALHNHYTQKISRSPGK 323

Search completed: June 18, 2001, 15:34:35  
 Job time: 243 sec

